

1/12

SEQUENCE LISTING

<110> Kabushiki Kaisha Hayashibara Seibutsu Kagaku Kenkyujo

<120> Cyclic maltosylmaltose, cyclic maltosylmaltose-forming enzyme, their preparation and uses

<130> 10102802

<160> 10

<210> 1

<211> 5

<212> PRT

<213> Arthrobacter globiformis

<400> 1

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<210> 2

<211> 583

<212> PRT

<213> Arthrobacter globiformis

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30

Gln Gly Asp Gly Glu Tyr Asp Pro Ser Asp Leu Gly Phe Tyr His Gly

35

40

45

Gly Asp Trp Ala Gly Leu Thr Asp Arg Leu Asp Tyr Ile Ala Asp Leu

50

55

60

Gly Val Thr Ala Ile Trp Leu Ser Pro Val Ser Glu Gln Gln Pro Leu

65	70	75	80
Ser Arg Asp Gly Leu Glu Ala Ser Tyr His Gly Tyr Phe Thr Arg Asp			
	85	90	95
Phe Ala Thr Pro Asn Glu His Phe Gly Asp Arg Ala Glu Leu Gln Glu			
	100	105	110
Leu Ile Asp Thr Ala His Asp Leu Gly Leu Lys Met Ile Leu Asp Val			
	115	120	125
Val Pro Asn His Thr Ala Asp Tyr Leu Ala Gly Thr Ser Thr Thr Tyr			
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Ser Pro Ser Thr Tyr Lys Pro Ala Ser Pro Leu Asp Asp Ala Ser Tyr			
145	150	155	160
Phe His His Ala Gly Asp Cys Leu Phe Asn Gly Leu Glu Thr Gln Thr			
	165	170	175
Gln Ile Glu Asn Cys Asp Leu Gly Gly Leu Asp Asp Leu Asp Gln Ser			
	180	185	190
Asn Pro Val Val Ser Ser His Leu Met Ser Thr Tyr Lys Asp Trp Val			
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Asp Met Gly Phe Asp Gly Ile Arg Val Asp Ala Ala Arg Ser Val Pro			
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Lys Pro Trp Leu Ala Asp Phe Glu Ala Glu Met Gly Val Pro Thr Phe			
225	230	235	240
Gly Glu Val Phe Val Gly Asp Val Asp Tyr Val Ser Glu Tyr Gln Asp			
	245	250	255
Tyr Glu Trp Gly Val Leu Asp Phe Pro Tyr Phe Phe Thr Val Arg Glu			
	260	265	270
Ala Phe Ser Ala Asp Thr Asp Met Asn Lys Leu Gly Asp Leu Phe Asp			
	275	280	285
Gln Asp Ser Lys Tyr Ala Asn Pro Asn Arg Leu Glu Thr Phe Leu Asp			
290	295	300	
Asn His Asp Arg Ala Arg Phe Leu Thr Trp Ala Asp Asp Asn Tyr Gln			
305	310	315	320
Arg Leu Arg Ser Gly Leu Thr Phe Leu Leu Thr Ser Arg Gly Val Pro			
	325	330	335
Val Ile Tyr Tyr Gly Thr Glu Gln Ala Asp Asp Gly Asn Gly Asn Pro			
	340	345	350

Tyr Glu Val Pro Ile Ala Asn Lys Asp Asn Arg Lys Asp Met Glu Ser
 355 360 365
 Phe Asp Gln Asn Ser Asn Leu Tyr Lys His Ile Gln Arg Leu Thr Ala
 370 375 380
 Ile Lys Ala Ala Tyr Pro Ala Leu Gln Val Gly Thr Gln Arg Glu Met
 385 390 395 400
 Trp Ser Asp Thr Ser Val Tyr Gly Phe Ser Arg Arg Val Asp Ser Thr
 405 410 415
 Gly Ala Glu Ala Met Thr Phe Ser Ser Asn Ser Trp Thr Thr Gln Thr
 420 425 430
 Arg Thr Val Pro Leu Arg Ala Glu Ser Ser Ile Thr Val Gly Thr Thr
 435 440 445
 Leu Thr Asn Leu Met Asn Thr Gly Asp Thr Val Thr Val Thr Ala Gly
 450 455 460
 Gly Val Thr Gly Lys Gln Ile Thr Val Ser Leu Gly Glu His Glu Ser
 465 470 475 480
 Lys Val Tyr Ala Pro Gly Thr Pro Val Ser Ala Tyr Ser Pro Glu Ala
 485 490 495
 Arg Asn Thr Thr Lys Ile Arg Val His Tyr Asn Val Gly Leu Gly His
 500 505 510
 Ser Ile Ala Ile Arg Gly Asp Glu Tyr Pro Phe Thr Trp Thr Ser Gly
 515 520 525
 Arg Gly Ala Arg Asn Val Ala Ser Asp Val Trp Glu Phe Glu Val Glu
 530 535 540
 Arg Ile Pro Asp Gly Glu Thr Phe Gln Phe Lys Pro Leu Ile Asp Asp
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 Val Thr Trp Ser Thr Gly Gly Asn Phe Thr Gly Thr Gly Gly Asp Val
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 Ile Asp Ile Tyr Pro Thr Phe
 580 583

<210> 3

<211> 1749

<212> DNA

<213> *Arthrobacter globiformis*

<400> 3

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tccgacctcg gtitttacct cggcggcgac tggcggggcc tgacggaccg gctcgactac	180
atcgccgacg tgggtgtgac ggcgatctgg ctctcgcccg tctccgagca gcagccgctc	240
tcgcgcgacg ggctggaggc cagctaccac ggctacttca ctcgggactt cgcgacgccg	300
aacgagcatt tcggcgaccg agccgagctg caggagctga tcgacacggc gcacgatctc	360
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acgttcctcg acaaccacga tcgggcgcgg ttcttcacct gggccgatga caactatcag	960
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<212> PRT

<213> *Arthrobacter globiformis*

<400> 4

His Ile Gln Arg Leu Thr Ala Ile Lys

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<210> 5

<211> 13

<212> PRT

<213> *Arthrobacter globiformis*

<400> 5

Asp Met Glu Ser Phe Asp Gln Asn Ser Asn Leu Tyr Lys

1

5

10

<210> 6

<211> 10

<212> PRT

<213> *Arthrobacter globiformis*

<400> 6

Leu Gly Asp Leu Phe Asp Gln Asp Ser Lys

1

5

10

<210> 7

<211> 27

<212> PRT

<213> *Arthrobacter globiformis*

<400> 7

Met Ile Leu Asp Val Val Pro Asn His Thr Ala Asp Tyr Leu Ala Gly

1

5

10

15

Thr Ser Thr Thr Tyr Ser Pro Ser Thr Tyr Lys

20

25

<210> 8

<211> 20

<212> PRT

<213> *Arthrobacter globiformis*

<400> 8

Asp Trp Val Asp Met Gly Phe Asp Gly Ile Arg Val Asp Ala Ala Arg

1

5

10

15

Ser Val Pro Lys

20

<210> 9

<211> 30

<212> PRT

<213> *Arthrobacter globiformis*

<400> 9

Tyr Ala Asn Pro Asn Arg Leu Glu Thr Phe Leu Asp Asn His Asp Arg

1

5

10

15

Ala Arg Phe Leu Thr Trp Ala Asp Asp Asn Tyr Gln Arg Leu

20

25

30

<210> 10

<211> 4467

<212> DNA

<213> *Arthrobacter globiformis*

<400> 10

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gtcgatctcg cgcagacgac ggaggagaaa cggtcgcagc gggaggcgct cgggctcgct	180
gtcgtcgagc agaacgcctc cgtcgccgat cctcggcgag ctgctcggac cgcacgagcc	240
cacctcgccc caggaccgtt catcgtgcac ctggacgtcg atgtgctgga ctctctcgac	300
gcaccccttg ccgagaacgt gaacggccga aacagcgggc cgaccgtcga gcagctgcgg	360

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ccgcgatcac gtctgacgt gaagcatcct gccgcgaagg gtcttgatgc gcatgcagta	780
cgggagtcga atcacattca cgggcacggc cgggtgcagt actigacaaa acgcatttat	840
acatgttgca tcatccagt aaaccgtgca gctcgcgagc cgaigcgcat ccgacaacga	900
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Met Arg Thr Thr Val Arg Thr Ala Arg Val Ser Ala	
1 5 10	
cgt acg ggc ctc gcg atg gga gca gcc gtc gcg ctg gcg gcc ggc gcg	999
Arg Thr Gly Leu Ala Met Gly Ala Ala Val Ala Leu Ala Ala Gly Ala	
15 20 25	
ctc acc tgg ggc acc ggc ccc gca ccc gcg agt gcc gac ccc acc acg	1047
Leu Thr Trp Gly Thr Gly Pro Ala Pro Ala Ser Ala Asp Pro Thr Thr	
30 35 40	
tcg ccc ggc ccg ctg gcc gag ggc gac gig atc tac cag gtg ctc gtc	1095
Ser Pro Gly Pro Leu Ala Glu Gly Asp Val Ile Tyr Gln Val Leu Val	
45 50 55 60	
gac cgg ttc gaa gac ggc gac ccc acc aac aac gac cag ggc gac gga	1143
Asp Arg Phe Glu Asp Gly Asp Pro Thr Asn Asn Asp Gln Gly Asp Gly	
65 70 75	
gag tac gat ccg tcc gac ctc ggt ttc tac cac ggc ggc gac tgg gcg	1191
Glu Tyr Asp Pro Ser Asp Leu Gly Phe Tyr His Gly Gly Asp Trp Ala	
80 85 90	
ggc ctg acg gac cgg ctc gac tac atc gcc gat ctg ggt gtg acg gcg	1239
Gly Leu Thr Asp Arg Leu Asp Tyr Ile Ala Asp Leu Gly Val Thr Ala	

95	100	105	
atc tgg ctc tcg ccc gtc tcc gag cag cag ccg ctc tcg cgc gac ggg			1287
Ile Trp Leu Ser Pro Val Ser Glu Gln Gln Pro Leu Ser Arg Asp Gly			
110	115	120	
ctg gag gcc agc tac cac ggc tac ttc act cgg gac ttc gcg acg ccg			1335
Leu Glu Ala Ser Tyr His Gly Tyr Phe Thr Arg Asp Phe Ala Thr Pro			
125	130	135	140
aac gag cat ttc ggc gac cga gcc gag ctg cag gag ctg atc gac acg			1383
Asn Glu His Phe Gly Asp Arg Ala Glu Leu Gln Glu Leu Ile Asp Thr			
145	150	155	
gcg cac gat ctc gga ctc aag atg atc ctc gac gtc gtg ccg aac cac			1431
Ala His Asp Leu Gly Leu Lys Met Ile Leu Asp Val Val Pro Asn His			
160	165	170	
acg gcc gac tac ctc gcg ggc aca tcg acg acc tat tcg ccg agc acc			1479
Thr Ala Asp Tyr Leu Ala Gly Thr Ser Thr Thr Tyr Ser Pro Ser Thr			
175	180	185	
tac aag ccg gcg agt ccg ctc gat gac gcg tcg tac ttc cat cac gcc			1527
Tyr Lys Pro Ala Ser Pro Leu Asp Asp Ala Ser Tyr Phe His His Ala			
190	195	200	
ggc gac tgc ctg ttc aac ggg ctc gag acg cag acc cag atc gag aac			1575
Gly Asp Cys Leu Phe Asn Gly Leu Glu Thr Gln Thr Gln Ile Glu Asn			
205	210	215	220
tgc gac ctc ggc ggg ctc gac gac ctc gat cag tcg aac ccg gtc gtc			1623
Cys Asp Leu Gly Gly Leu Asp Asp Leu Asp Gln Ser Asn Pro Val Val			
225	230	235	
tcg tcg cac ctg atg agc acg tac aag gac tgg gtc gac atg ggc ttc			1671

Ser Ser His Leu Met Ser Thr Tyr Lys Asp Trp Val Asp Met Gly Phe	
240 245 250	
gac ggc atc cgg gtc gat gcg gcg cgc tcg gtg ccg aag ccg tgg ctc	1719
Asp Gly Ile Arg Val Asp Ala Ala Arg Ser Val Pro Lys Pro Trp Leu	
255 260 265	
gcc gac ttc gaa gcc gag atg ggc gtg ccg acc ttc ggc gag gtg ttc	1767
Ala Asp Phe Glu Ala Glu Met Gly Val Pro Thr Phe Gly Glu Val Phe	
270 275 280	
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Val Gly Asp Val Asp Tyr Val Ser Glu Tyr Gln Asp Tyr Glu Trp Gly	
285 290 295 300	
gtg ctc gac ttc ccc tac ttc ttc acg gtg cgc gag gcg ttc tcg gcc	1863
Val Leu Asp Phe Pro Tyr Phe Phe Thr Val Arg Glu Ala Phe Ser Ala	
305 310 315	
gat acc gac atg aac aag ctc ggc gac ctc ttc gac cag gac agc aag	1911
Asp Thr Asp Met Asn Lys Leu Gly Asp Leu Phe Asp Gln Asp Ser Lys	
320 325 330	
tac gcg aac ccg aac cgg ctg gag acg ttc ctc gac aac cac gat cgg	1959
Tyr Ala Asn Pro Asn Arg Leu Glu Thr Phe Leu Asp Asn His Asp Arg	
335 340 345	
gcg cgg ttc ctc acc tgg gcc gat gac aac tat cag cgg ctg cgc tca	2007
Ala Arg Phe Leu Thr Trp Ala Asp Asp Asn Tyr Gln Arg Leu Arg Ser	
350 355 360	
gga ctg acg ttc ctc cta acc tcc cgg ggc gtg ccc gtg atc tac tac	2055
Gly Leu Thr Phe Leu Leu Thr Ser Arg Gly Val Pro Val Ile Tyr Tyr	
365 370 375 380	

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Gly Thr Glu Gln Ala Asp Asp Gly Asn Gly Asn Pro Tyr Glu Val Pro	
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Ile Ala Asn Lys Asp Asn Arg Lys Asp Met Glu Ser Phe Asp Gln Asn	
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Ser Asn Leu Tyr Lys His Ile Gln Arg Leu Thr Ala Ile Lys Ala Ala	
415 420 425	
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Tyr Pro Ala Leu Gln Val Gly Thr Gln Arg Glu Met Trp Ser Asp Thr	
430 435 440	
tcc gtc tac ggg ttc tcg cga cgc gtc gac agc acg ggt gcc gag gcg	2295
Ser Val Tyr Gly Phe Ser Arg Arg Val Asp Ser Thr Gly Ala Glu Ala	
445 450 455 460	
atg acc ttc tcg tcg aac tcg tgg acg acg cag acg cgc acg gtg ccg	2343
Met Thr Phe Ser Ser Asn Ser Trp Thr Thr Gln Thr Arg Thr Val Pro	
465 470 475	
ctg cgc gcc gag agc tcg atc acg gtc ggt acg acg ctg acg aac ctc	2391
Leu Arg Ala Glu Ser Ser Ile Thr Val Gly Thr Thr Leu Thr Asn Leu	
480 485 490	
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Met Asn Thr Gly Asp Thr Val Thr Val Thr Ala Gly Gly Val Thr Gly	
495 500 505	
aag cag atc acc gtc tcc ctc ggc gag cac gag agc aag gtc tat gcg	2487
Lys Gln Ile Thr Val Ser Leu Gly Glu His Glu Ser Lys Val Tyr Ala	
510 515 520	

ccc ggc acc ccg gta tcg gca tac agc ccc gaa gcg cgc aac acc acg 2535
Pro Gly Thr Pro Val Ser Ala Tyr Ser Pro Glu Ala Arg Asn Thr Thr
525 530 535 540

aag atc cgc gtg cac tac aac gtg ggc ctc ggg cac agc atc gcg atc 2583
Lys Ile Arg Val His Tyr Asn Val Gly Leu Gly His Ser Ile Ala Ile
545 550 555

cgc ggc gac gag tac ccg ttc acc tgg acc tcc ggc cga ggc gcg cgc 2631
Arg Gly Asp Glu Tyr Pro Phe Thr Trp Thr Ser Gly Arg Gly Ala Arg
560 565 570

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 Asn Val Ala Ser Asp Val Trp Glu Phe Glu Val Glu Arg Ile Pro Asp
 575 580 585

ggt gag acc ttc cag ttc aag cct ctg atc gac gac gtc acc tgg tcg 2727
 Gly Glu Thr Phe Gln Phe Lys Pro Leu Ile Asp Asp Val Thr Trp Ser
 590 595 600

acc ggc ggc aac ttc acc ggg acg ggc ggc gac gtg atc gac atc tac 2775
Thr Gly Gly Asn Phe Thr Gly Thr Gly Gly Asp Val Ile Asp Ile Tyr
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ccc acc ttc tga accatccct cccgggactc caccgaaagg atgcttgtga gccac 2832
Pro Thr Phe

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